P AAF72416



Sequences producing High-scoring Segment Pairs: Frame Score Match Pct E-val 1 P_AAF72416 Human PRO302 cDNA. 1650 1650 100 0.0 + 2 P_AAF30502 Human PRO302 cDNA clone DNA40370-1217. 1650 1650 100 0.0 3 P_AAA13199 PRO302, vitellogenic carboxypeptidase ho + 1650 1650 100 0.04 P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. + 1650 1650 100 0.0 5 P_AAX25445 Human PRO216 cDNA clone UNQ265. + 1650 1650 100 0.0 6 AX098272 Sequence 11 from Patent WO0119987. + 1650 1650 100 0.0 1646 100 7 NM_021626 Homo sapiens serine carboxypeptidase 1 p + 1640 0.0 Homo sapiens serine carboxypeptidase 1 p + Homo sapiens cDNA FLJ14467 fis, clone MA + 8 AF282618 1646 100 1640 0.0 9 AK027373 1637 1640 100 0.0 Homo sapiens MSTP034 mRNA, complete cds. + 1594 1594 100 10 AF113214 0.0 11 P_AAC75884 Human ORFX ORF1439 polynucleotide sequen + 1543 1619 99 0.0 >1 P_AAF72416 Human PRO302 cDNA. (1650 bp) [1 seg] Score = 1650 (3271 bits), Expect = 0.0Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+ DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCGCACTGCGGCGCTCTCCC $1 \ \ \mathsf{GCCTGTTGCTGATGCTGCGTGCGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC}$ P_AAF72416 DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCCGCTGCTGGTGGGCCTGAACGCAGGAGCTGTCATT P_AAF72416 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCATT CENI DNA40370 121 GACTGGCCCACAGAGGAGGCCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC NTER TER P_AAF72416 121 GACTGGCCCACAGAGGAGGCCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC DNA40370 131 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC ********** P AAF72416 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC DNA40370 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG P AAF70416 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG DNA40370 301 GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC P_AAF72416 301 GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT P_AAF72416 $3\,61$ AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC P_AAF7::416 $481\ {\tt TTUAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA}$ DNA40370 P_AAF72416 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA DNA40370 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC P_AAF72416 541 GGAAAAATGGCAGCTGGCATTGGTUTAGAGUTTTATAAGGCCATTCAGCGAGGGACCATC DNA40370 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCCTGTTGATTCGCTG

601 AAGTGCAACTTIGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCCTGTIGATTCGGTG

DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
P_AAF72416	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAF73416	731	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGC'I'G'I'GGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
P_AAF72416	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAF72416	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAF72416	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATC
P_AAF72416	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGGAAGCTCAAAATTATTCCTGAGGATCAATC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGT
P_AAF73416	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGT
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACA
P_AAF72416	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACA
DNA40370		CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA **********************************
P_AAF7::416	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370		GAAC'IGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG *********************************
P_AAF72416	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370		GAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT ************************************
P_AAF72416	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370		GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGATGAGACTGGTGACT ************************************
P_AAF73416	13.21	GGTCATATGCTTCCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370	1381	CAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
P_AAF77416	1331	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGCCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
P_AAF7.:416	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
DNA40370] [[[GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
P_AAF72416	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1501	TGGAAATTA PPPCTGCTTCTFAAAAAAAACCTAAGAT PTTETAAAAAATIGA ETTGTTTTG
the bibliography		
P AAF72416	1561	TGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

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1621 ATCAAAATAAAGGATGATAATAGATATTAA
          1621 ATCAAAATAAAGGATGATAATAGATATTAA
P AAF72416
>2 P_AAF30502 Human PRO302 cDNA clone DNA40370-1217. DNA, PAT 29-MAY-2001 (1650
bp) [1 seg]
 Score = 1650 (3271 \text{ bits}), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+
 DNA40370
             1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
P AAF30502
             1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
 DNA40370
            61 GTCCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
P AAF30502
            61 GTCCCGCGGTGCTTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
 DNA40370
           121 GACTGGCCCACAGAGGAGGCCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
               P_AAF30502
           121 GACTGGCCCACAGAGGAGGCCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
           181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
 DNA40370
              P AAF30502
           181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
 DNA40370
           241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
               ***********
           241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
P_AAF30502
 DNA40370
           301 GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
P AAF30502
           301 GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
 DNA40370
           361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
               P AAF30502
           361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
 DNA40370
           421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
               421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P AAF30502
 DNA40370
           481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
P AAF30502
           481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
 DNA40370
           541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
P_AAF30502
           541 -GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
 DNA4037:1
           601 AAGTSCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
               *********
P_AAF305011
           6001 AAGTSCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
 DNA40370
           661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
              P_AAF30501
           661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
           721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTÄAATAAGGGGCTCTACAGAGAGGCC
 DNA40370
              P AAF30502
           721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGUCGTAAATAAGGGGCTCTACAGAGAGGCC
 DNA40570
           78! ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
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P_AAF30502	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
DNA40370	8.11	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAF3050.	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAF3050.	901	CAGAGCCACCTAGTTTGTCTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAF30502	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAF30502	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACA
P_AAF30502	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACA
DNA40370	1141	
P_AAF30502	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTT
P_AAF30502	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTT
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAF30502	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
DNA4037()	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
P_AAF3050:	1321	
DNA40370	1381	CAGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
P_AAF30502	1381	CAGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
P_AAF30502	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
P_AAF3050::	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
P_AAF3050::	1061	TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTGTTTTG
DNA40370	162:1	ATCAAAATAAAGGATGATAAATAAA
P_AAF30501	1621	ATCAAAATAAAGGATGATAATAGATATTAA
sequence. (1650_b 50_(32	0302, vitellogenic carboxypeptidase homologue nucleotide op) [1 seg] 071 bits), Expect = 0.0 00/1650 (100%), at 1,1 1650,1650, Strand +/+
DNA40370	1	GCCTGTTGCTGATGCTGCTGCTGCTGCTTGTTCATGGAGCTGGCACTGCGCACTCCCC

P_AAA13199	1	**************************************
DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
P_AAA13199	61	$\tt GTCCCGCGGTGGTTGCTGCTGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT$
DNA40370	121	GACTGGCCCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
P_AAA13199	1.21	${\tt GACTGGCCCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC}$
DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
P_AAA13199	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG *********************************
P_AAA13199	241	$\tt CTGGTCATGTGGCTTCAGGGGGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGGGGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGGGGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGGGGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGGGGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGGGGGTCCAGGGTGTTTGGAAACTTTGAGGGGGGTTCTAGCACTGGATTTGGAAACTTTGAGGGGGGTCCAGGGTGTTGGAAACTTTGAGGGAAACTTTGAGGAAAACTTTGAGGAAACTTTGAGGAAACTTTGAGGAAACTTTGAGGAAAACTTTGAGGAAAACTTTGAGGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAAAAAA$
DNA40370	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC ********************************
P_AAA13199	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCA
DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGG
P_AAA13199	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAACATCCT
P_AAA13199	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGCCTT
DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATGGA
P_AAA13199	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
P_AAA13199	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
DNA4037()	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
P_AAA13199	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
DNA4037()	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
P_AAA13199	651	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAA13199	721	$\tt GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCC$
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACAGAGATGGGGTGAACTTC
P_AAA13199	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAAls199	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGFTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAA13199	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DMA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

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P_AAA13199	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC	
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC	
P_AAA13199	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC	
DNA40370	1031	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG	
P_AAA13199	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG	
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA	
P_AAA13199	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA	
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG	
P_AAA13199	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG	(
DNA40370		GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGC	
P_AAA13199	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT	
DNA40370	1321		
P_AAA13199	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT	
DNA40370		CAGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT	
P_AAA13199	1381	CAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT	
DNA40370 P AAA13199		GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCA'TTCTTCCC'TGTATC'TAACTGGGGCTGT *****************************	
DNA40370		GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGGTAAAATCATTGTCTCTGGAGGCAATT	
P_AAA13199		**************************************	
DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTTTG	
P_AAA13199	1561	TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTTTG	
DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA	
P_AAA13199	1621	ATCAAAATAAAGGATGATAATAGATATTAA	
(1650 bp) [: Score = 165	1 seg] 50 (32	otein PRO302 cDNA clone DNA40370-1217. ENA, PAT 25-JUN-1999 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+	
DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC	
P_AAX52258	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC	
DNA40370	61	GTCCCGCGCTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT	
P_AAX52258	6.1	GTCCCGCGCTGGTTGCTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCATT	
DNA4(1370	121	GACTGGCCCACAGAĞGAĞGGCAAĞGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC	
P_AAX52258	121	GACTGGCCCACAGAGGGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC	

DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
P_AAX52258	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
P_AAX52258	241	$\tt CTGGTCATGTGGCTTCAGGGGGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG$
DNA40370	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
P_AAX52258	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
P_AAX52258	361	${\tt AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT}$
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX52258	421	${\tt GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC}$
DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
P_AAX52258	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
DNA40370	541	GGAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
P_AAX52258	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
P_AAX50258	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX52258	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	731	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX52258	731	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC *********************************
P_AAX52258	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX52.158	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX5::::58	901	CAGAGCCACCTAGTTTGTCTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370		AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAX5258	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
DNA40470	10.:1	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAX52::58		$\tt TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC$
DNA40570	1051	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGTGATCAACGTGACGGTGTATAATTGGACAG
P AAX52258	1031	$\tt ATTAGCATTGTGGAGGGTTGCTGGAGGGCAG+SATGAAGGTGAGGGTGTATAATGGAGAG-SATGAGGAGGGTGTATAATGGAGAGGGGAGGG$

DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
P_AAX5.2258	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
P_AAX52258	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAX52258	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
P_AAX52258	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370	1381	CAGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
P_AAX52258	1381	CAGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****************************
P_AAX52258	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT **********************************
P_AAX52258	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1561	TGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTTT
P_AAX52258	1561	TGGAAATTATTTCTGCTTCTTAAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTTTT
DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA ************
DNA40370 P_AAX52258		
P_AAX52258 >5 P_AAX254 Score - 16	1621 45 Hur 50 (32	**********
P_AAX52258 >5 P_AAX254 Score - 16	1621 45 Hur 50 (32 = 165	**************************************
P_AAX52258 >5 P_AAX254 Score - 16 Identities	1621 45 Hur 50 (32 = 165	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370	1621 45 Hur 50 (32 = 165 1	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC ************************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445	1621 45 Hur 50 (32 = 165 1 1	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGCGCTCTCCC ***********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370	1621 45 Hur 50 (32 = 165 1 1 61	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGCGCTCTCCC **********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370 P_AAX25445	1621 45 Hur 50 (32 = 165 1 1 61 61 121	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGGGCTCTCCC **********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370	1621 45 Hur 50 (32 = 165 1 1 61 61 121	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGCGCTCTCCC **********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445	1621 45 Hur 50 (32 = 165 1 1 61 61 121 121 181	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGCGCTCTCCC ***********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370	1621 45 Hur 50 (32 = 165 1 1 61 61 121 121 131	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGCGCTCTCCC ***********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445	1621 45 Hur 50 (32 = 165 1 1 61 61 121 121 131 241	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCGCACTGCGGGCGCTCTCCC **********************
P_AAX52258 >5 P_AAX254 Score - 16 Identities DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370 P_AAX25445 DNA40370	1621 45 Hur 50 (32 = 165 1 61 61 121 131 131 241	ATCAAAATAAAGGATGATAATAGATATTAA man PRO216 cDNA clone UNQ265. (1650 bp) [1 seg] 271 bits), Expect = 0.0 50/1650 (100%), at 1,1-1650,1650, Strand +/+ GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGGACTGCGGGCGCTCTCCC **********************

DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
P_AAX25445	361	${\tt AGTCTCCTATTTGTGGATAATCCCGTGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT}$
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX25445	421	GCCTATGCCAAGGACCTGGCTATGGTTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
P_AAX05445	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
P_AAX25445	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
P_AAX25445	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX25445	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA-10370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX25445	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA-10370	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACAGATGGGGTGAACTTC
P_AAX::5445	781	${\tt ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC}$
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX.:5445	841	${\tt TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA}$
DNA-10370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX::5445	901	${\tt CAGAGCCACCTAGTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA}$
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAX.:5445	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAXU5445	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTGTGGACGGGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
P_AAX 5445	1031	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA49370	1141	CTGGATCTCATCGTAGATACCATGGGTEAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
P_AAX.15445	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
P_AAX25445	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAX25445	1261	GAAACATCTGCTT FTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
P_AAX25445	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGAGACTGGTGACT
DNA40370	1381	CAGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
P_AAX25445	1381	CAGCAAGAATAGGATGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
P_AAX25445	1441	**************************************
DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
P_AAX25445	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
P_AAX25445	1561	TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTTT
DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA
P_AAX25445	1621	ATCAAAATAAAGGATGATAATAGATATTAA
>6 AX098272	Segu	ence 11 from Patent W00119987. (1650 bp) [1 seg] 271 bits), Expect = 0.0
Identities	= 16	50/1650 (100%), at 1,1-1650,1650, Strand +/+
DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
AX098272	1	GCCTGTTGCTGATGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
AX098272	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
DNA40370	121	GACTGGCCCACAGAGGAGGCCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
AM098272	1.21	GACTGGCCCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
AX098.272	181	${\tt TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC}$
DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
AX098272	241	$\tt CTGGTCATGTGGCTTCAGGGGGGTTCCAGGGGGTTCTAGCACTGGATTTGGAAACTTTGAG$
DNA40370	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
AX098117.1	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
DHA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
AX093272	361	${\tt AGTCTCCTATPTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT}$
DNA40370	40:1	GCCTATGCCAAGGACCTGGCTATGGIGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
AX098272	43:1	$\tt GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC$
DNA40 +70	481	$\tt TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGACTCCTATGGACTCCAGACTCCTATGGACTCCAGACTCCTATGGACTCCAGACTCCCAGACTCAGACTCCAGACTCAGACTCCAGACTCAGACTCCAGACTCAGACAACAACAACAACAACAACAACAACAACAACAACAA$
AX098272	48!	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTGTACATTTTTCTCAGAATCCTATGGA

DNA40370	541	GGAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGACCATC
AX098272	5.11	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
AX098272	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
AX098272	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
AX098272	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
AX098272	781	ACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
AX098272	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
AX098272	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
AX098272	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
AX098272	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
AX098272	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
AX098271	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
AX098272	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
AX098272	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370	1 . 21	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
AX098272	1521	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTTGGCCTTTGGGGCACAGAGCT
AX098272	1581	CAG PAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
AX098272	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

DNA40370	150	1 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
AX098272	150	**************************************
DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
AX098272	1561	1 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
DNA4037()	1621	L ATCAAAATAAAGGATGATAATAGATATTAA
AX098272	1621	ATCAAAATAAAGGATGATAATAGATATTAA
(L = • • • • • •	no sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
Identities	5 = 16	251 bits), Expect = 0.0 46/1648 (99%), at 2,1-1649,1648, Strand +/+
DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
NM_021626	1	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
DNA40370	62	TCCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
NM_021626	61	TCCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
DNA40370	132	ACTGGCCCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
NM_021626	121	ACTGGCCCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
DNA40370	183	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
NM_021626	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGG
NM_021626	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTTGGAAACTTTGAGG
DNA-10370	300	AAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCA
NM_021626	301	AAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCA
DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTG
NM_001626	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTG
DNA40370	422	CCTATGCCAAGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
NM_021626	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
DNA-10370	483	TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG
NM_0.11626	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAG FCCTATGGAG
DNA 10370	543	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCA
NM_031626	5.11	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCA
DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGC
NM_021626	601	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCCGTGGATTCGGTGC
DNA40370	662	fcTcCTggggaCcTTaCCTgTaCagGaTgTCTCTCTCgaagaCaaaggTCTggCagagg
NM 021626	661	: CTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTČGAAGACAAAGGTCTGGCAGAGG

DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
NM_021626	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT
NM_021626	781	${\tt CAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT}$
DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
NM_021626	841	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
NM_021626	901	${\tt AGAGCCACCTAGTTTGTCATCTGCGCCACGTGAGACACCTACAACGAGATGCCTTAA}$
DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
NM_021626	961	${\tt GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT}$
DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
NM_021626	1021	${\tt GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA}$
DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
NM_021626	1081	${\tt TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC}$
DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
NM_021626	1141	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
NM_021626	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
DNA40370		AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
	1363	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG ***********************************
DNA40370	1363 1261	****************
DNA40370 NM_0216.26	1262 1261 1323	**************************************
DNA40370 NM_0216.26 DNA40370	1262 1261 1323 1301	**************************************
DNA40370 NM_021626 DNA40370 NM_021626	1262 1261 1322 1321 1382	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_0216.26 DNA40370 NM_0216.26 DNA40370	1262 1261 1323 1321 1382 1381	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_021636 DNA40370 NM_021636 DNA40370 NM_021626	1262 1261 1323 1321 1382 1381 1442	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626 DNA40370	1262 1261 1323 1321 1382 1381 1442 1441	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_021636 DNA40370 NM_031636 DNA40370 NM_021626 DNA40370 NM_031636	1262 1261 1323 1321 1382 1381 1442 1441	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626 DNA40370	1262 1261 1322 1321 1382 1381 1442 1441 1502	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626	1262 1261 1322 1321 1382 1381 1442 1441 1502 1501	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************
DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_021626 DNA40370 NM_0.21626 DNA40370 NM_0.21626	1262 1261 1322 1321 1382 1381 1442 1441 1502 1501 1562	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAAGCTG GTCATATGGTTCCTTCTGACCAAGGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC **********************************

>8 AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1) (1921 bp) [1 seq] Score = 1640 (3251 bits), Expect = 0.0Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+ 2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG DNA40370 AF282618 ${\tt L} {\tt CCTGTTGCTGATGCTGCGTGCGGTACTTGTCATGGAGCTGCGGCACTGCGGCGCTCTCCCG}$ DNA40370 6.2 TCCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG £1 TCCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG AF282618 DNA40370 122 ACTGGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT ****************** AF282618 121 ACTGGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT DNA40370 182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC ****************** AF282618 181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC DNA40370 242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGG ****************** 241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGG AF282618 DNA40370 302 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCA AF383618 301 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCA DNA40370 362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTG AF.18.1618 361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTG DNA40370 422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT AF282618 421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT DNA40370 432 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG **************** AF282618 481 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG DNA40370 542 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCA AF282618 541 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCA DNA40370 601 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGC AF282618 601 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCCGTGGATTCGGTGC DN440370 66.2 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG ************ AF::32618 661 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG DNA40370 722 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGGCTCTACAGAGAGGGCCA *********** AFT 37618 DM: 10370 732 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT ******** AF: 32618 781 CAGAGCTGTGGGGGAAAGCAGAAATGATTATTGAACAGAACACAGATGGGGTGAACTTCT DNA40370 842 ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC

AF28.1618	8.11	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC	
DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA	(
AF282618	901	AGAGCCACCTAGTTTGTCTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA	ļ
DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT	-
AF28.2618	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT	(
DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA	(
AF282618	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA)
DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC	<
AF282618	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC	(
DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG	
AF282618	1141	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG	
DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG	
AF282618	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG	
DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG	
AF282618	1261	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG	
DNA40370	1322	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC	
AF282618	1321	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC	
DNA40370	1382	AGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG	
AF282618	1381	AGCAAGAATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG	
DNA40370	1442	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG	
AF282618	1441	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG	
DNA40370	1502	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT	
AF282618	1501	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT	
DNA40370	1562	GGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTGTA	
AF282618	1561	GGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTGTTTTGA	
DNA40370	1622	TCAAAATAAAGGATGATAATAA	
AF280618	1621	TCAAAATAAAGGATGATAACAGATATTA	
>9 AF017373 [1 seg]	Homo	sapiens cDNA FLJ14467 fis, clone MAMMA1000672, weakly (1641 bp))
Score = 16	37 (32 - 164	45 bits), Expect = 0.0 0/1641 (99%), at 8,1-1648,1641, Strand +/+	
DNA40370	Š	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGGCGCTCTCCCGTCCCGC	
AF927373	1	GC FGATGCTGCCGTGCGGTAC1TGTCATGGAGGGGGACTGCGGGGGGCTCTCCCGTCCCG	
DNA40370	63	GGTGGTTGCTGC : SCTGCCGCT GCTGCTGGGGCCTGAACGCAGGAGCTGTCAT TGACTĞGC	

61	L GGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
128	CCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
121	CCACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
188	TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCA
181	TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCA
248	TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGAAATTG
241	$. \ \ TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGGAAATTG$
308	GGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCC
301	GGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCC
368	TATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATG
361	${\tt TATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATG}$
428	CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
421	CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
488	GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAA
481	GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
548	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCA
541	
608	ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT
601	ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT
668	GGGGACCTTACCTGTACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
661	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
728	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
721	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCCTCTACAGAGAGGCCACAGAGC
788	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACA
781	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACA
8::3	TC PTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTC
841	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
9113	ACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
901	ACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
961	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAT
1023	GCCAGGCTACCAACGTCTTTGTGAACATSGAGGAGGACTTGATGAAGGCAGTCATTAGCA
	128 121 188 181 248 241 308 301 368 361 428 421 488 481 548 541 608 661 728 731 788 731 843 841 903 901 968

AK027373	1021	$\tt GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA$
DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
AK027373	1081	$\tt TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC$
DNA40370	1148	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
AK027373	1141	${\tt TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC}$
DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
AK027373	1201	$\tt CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT$
DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
AK027373	1261	$\tt CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA$
DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
AK027373	1321	$\tt TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG$
DNA40370	1388	AATAGGATGGATGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
AK027373	1381	${\tt AATAGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGGCTGAGAGCTGAGAGAGA$
DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
AK027373	1441	${\tt GGCCGCTGAAGCTGTAGGAAGCGCCACTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG}$
DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
AK027373	1501	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
DNA40370	1568	${\tt TATTTCTGCTTCTTAAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTGTTTTGATCAAAA}$
AK027373	1561	${\tt TATTTCTGCTTCTTAAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA}$
DNA-10370	1628	TAAAGGATGATAATAGATATT
AK0.17373	1621	TAAAGGATGATAATAT
(1902 bp) [Score = 15	1 seg] 94 (31	o sapiens MSTP034 mENA, complete cds. mRNA, PRI 12-DEC-2000 60 bits), Expect = 0.0 94/1594 (100%), at 56,1-1649,1594, Strand +/+
DNA40370	56	CTCCCGTCCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTG
AF113214	1	CTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTG
DNA40370	116	TCATTGACTGGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
AF113214	61	TCATTGACTGGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
DNA40370	176	ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
AF113214	121	ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
DNA40370	236	TGCCCCTGGTCATGTGGCTTCAGGGGGGTCCAGGGGGTTCTAGCACTGGATTTGGAAACT
AF113214	181	TGCCCCTGGTCATGTGGGCTCCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACT

DNA40370	296	TTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGG
AF113214	2.41	$\tt TTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGG$
DNA40370	356	CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTA
AF113214	301	$\tt CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTA$
DNA40370	416	GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
AF113214	361	GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
DNA40370	476	CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT
AF113214	421	${\tt CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT}$
DNA40370	536	ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGA
AF113214	481	ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGA
DNA40370	596	CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATT
AF113214	541	$\tt CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATT$
DNA40370	656	CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTC
AF113214	601	$\tt CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG$
DNA40370	7.1.6	CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
AF113::14	661	CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
DNA40370	776	AGGCACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGA
AF113214	721	AGGCCACAGAGCTGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGA
DNA40370	836	ACTTCTATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAAT
AF113214	781	ACTTCTATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAAT
DNA40370	896	TCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATG
AF113214	841	TCACACAGAGCCACCTAGTTTGTCTTGTCAGCGCCACGTGAGACACCTACAACGAGATG
DNA40370	956	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATC
AF113214	901	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGCACACAAAATTATTCCTGAGGATC
DNA40370	1016	AATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
AF113214	961	AATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
DNA40370	1076	CAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
AF1132114	1021	CAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
DNA40370	1136	GACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGT *********************************
AF113214	1081	GACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGT
DNA40370	1196	GGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAAT
AF113214	1141	GGCCAGAACTGCCTAAATTCAGPCAGCTGAAGTGGAAGGCCCTGPACAGTGACCCTAAAT

DNA40370 AF113214		CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA ************************************
DNA40370		
		AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG ***********************************
AF113214		AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
DNA40370	1376	**************************************
AF113214	1321	TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
DNA40370	1436	GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
AF113214	1381	GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
DNA40370	1496	GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
AF113214	1441	GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
DNA40370	1556	CAATTTGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTG
AF113214	1501	CAATTTGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAAATTGATTTG
DNA40370	1616	TTTTGATCAAAATAAAGGATGATAATAGATATTA
AF113214	1561	TTTTGATCAAAATAAAGGATGATAATAGATATTA
bp) [1 seg] Score = 15	43 (30	uman ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. (1921 059 bits), Expect = 0.0
Identities	= 16.	19/1642 (98%), Gaps = $3/1642 (0%)$, at $8.2-1649.1640$, Strand +/+
DNA40370		GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
	8	
DNA40370	8	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
DNA40370 P_AAC75884	8 2 68	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC *****************
DNA40370 P_AAC75884 DNA40370	8 2 68 62	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC *****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884	8 2 68 62 138	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370	8 2 68 62 138 133	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC *****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884	8 2 68 62 138 132 188	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370	8 68 62 128 123 183	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884	8 68 62 138 133 183 183 248	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370	8 2 68 62 128 123 183 183 248	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884	8 2 68 62 128 122 188 181 248 239	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370	8 68 62 128 122 188 182 248 239 308 299	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884 DNA40370 P_AAC75884	8 68 62 128 122 188 182 248 249 308 299	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC ****************
DNA40370 P_AAC75884	8 68 62 128 122 188 182 248 249 308 299 368 359	GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGCGCCGCCCCCCCC

DNA40370	488	GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAA
P_AAC75884	479	GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
DNA40370	548	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCA
P_AAC75884	539	
DNA40370	608	ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCT
P_AAC75884	599	${\tt ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT}$
DNA40370	668	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
P_AAC75884	659	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
DNA40370	728	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
P_AAC75884	719	${\tt AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC}$
DNA40370	788	TGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACA
P_AAC75884	779	TGTGGGGGAAAGCAGAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACA
DNA40370	848	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
P_AAC75884	839	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
DNA40370	908	ACCTAGTTTGTCTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
P_AAC75884	899	ACCTAGTTTGTCTCTGTCAGCGCCACGTGAGACACCTACAACGAGACGCCTTAAGCCAGC
DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
P_AAC75884	959	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
P_AAC75884	1019	${\tt GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATCGACA}$
DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
P_AAC75884	1079	${\tt TTGTGGATACGTTGCTGGAGGCAGGGGTCAATGTGACTGTATAATGGGCAGCTGGATC}$
DNA40370	1148	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
P_AAC75884	1139	${\tt TCATTGTGGACACCATAGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGT}$
DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
P_AAC75884	1199	$\tt CCAGATTCAATCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT$
DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
P_AAC75884	1259	$\tt CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA$
DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
P_AAC75884	1319	${\tt TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGGACTGGTGACTCAGCAAG}$
DNA40370	1389	AATAGGATGGATGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
P AAC75884	1370	AATAGGATGGATGĞGGCTGGAGATGAGCTGGTTTGGCCTTGGGGÇACAĞAGCŢĞAGCTGA

DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
P_AAC75884	1439	
DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
P_AAC75884	1499	${\tt AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT}$
DNA40370	1568	TATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
P_AAC75884	1559	${\tt TATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTTTTGATCAAAA}$
DNA40370	1628	TAAAGGATGATAATAGATATTA
P_AAC75884	1619	TAAAGGATGATAATAGATATTA



Tue Jue MADAW 5:03 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI] /home/ruby/va/Molb:0/carpenda/templ/pl.DuA40370 (452 aa)

Sequences pr 1 F_AAB802 2 F_AAB203 3 F_AAT853 4 F_AAT133 5 P_AAT057 6 AAG16632 7 NP_06763 8 P_AAB416 9 AAG39285	55 41 78 87 68 .1 9.1 75	ing High-scoring Segment Pairs: Human PF0302 protein - Homo sapiens. Human PF0302 - Homo sapiens. PF0302, vitellogenic carboxypeptidase hom protein PF0302 - Homo sapiens. Human PF0310 (vitellogenic carboxypeptida serine carboxypeptidase 1 precursor prote serine carboxypeptidase 1 precursor prote Human ORFX ORF1439 polypeptide sequence S MSTP034 - Homo sapiens	Score 2382 2382 2382 2382 2382 2382 2382 2316	Match 450 450 450 450 450 450 450 439 400	100 100 100 100 100 100 100	E-val 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
Score = 238	82 (!	man PE0302 protein - Homo sapiens. (451 aa) 922 bits), Expect = 0.0 2/452 (100%), Fositives = 452/452 (100%), a			2	
DNA40370		L MELALPESPYPEWLLLLFLLLGLNAGAVIDWPTEEGKEVWD	YVTVFE	(DAYMFWI	√LYYA	.TN
P_AAB30055		**************************************				
DNA40370		SCKNFSELFLVMWLOGGFGGSSTGFGHFEETGPLDSHLKPRF	arrwit a	A CLIEVA	IDNEV	сm
P AABBOUSS		**************************************	* * * * *	* * * * * * *	* * * *	* *
DNA40370		GFSYVNGSGAYAKCLAMZASDWMVLUKTEESCHKRECTUDEV	arara	VCC [11] 7	ובי דיביו	te t
P AAB80255		* * * 4 * * * * * * * * * * * * * * * *	* * * * *	* * * * * *	* * * *	* *
		GFCYVII 3SGAYAKDLAMVASI MIIVLLETFESCHKEFQTVPFY				
DNA40+7)	151	YKAI@FGTIKONFAGVALGESWIGPVISVLSWGPYLYSMSLI	EDRGL.	AEVSFVA	EQVLI	NA * *
P_AAB((), (5))	181	YKAIĢEGTIECNFAGVALODSWIJPVOSVLSWGPYLYSMSLL				
DNA40 +7	241	YNEGETREATELWGKAEMETEONTDSVNFYNILTKSTPTSTM	EJSLE:	FTQSHLV	CLCQI	RН
P_AAB80.:5 +	241	VNEGI VREATELWGKAENLI EQNIDÖVNEYNILIKSIPISIM				
DNA40 (7)	301	VEHL DEDALSOMMISELEEKLELEEERDSWGGQATNVEVNME	EDENIK	PVISIVD	ELLEA	AG
P_AAB801155	301	VEHIQE DALSQLMNGPIEFELEII PELQSWGGQATNVFVNME				
DNA4(57g)		IN/TTYNGOLD. INDTMG: EAWVERLEWPELPHESOLKWHAL	YSEPEC	ALETSAF	VE'SYE	(N)
P_AAB80255	561	INVTVINGQLD: EVDTMGCRAWVRKIKWPELPKFSQLKWKAL				
DNA40370		LAFYWILKAGEOMESDOG: MALKMMRI.WTOOE				
P_AAP#021/	421	LARTWILKA SENVERBOGS MALKMMELVTOOE				
>2 P AAB20:41	Hanic	of FROUND - Lomb sap ons. (452 aā) [1 seq]				
Score = 2382	2 (9)	's lifts), Emperer				
Laentiti://	45.17	7450 (1907) Fraintee 4527458 (1907), at	1,1-4	1, 2, 4, 2,		
DNA4011	; I	MEDALESELE DE ESELUCIO DE LA SAVIONE DE ESERVINAS AS	eter en	AYNEWE	TYAT	

P_AAB20341	1	MELALPFSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKEAYMFWWLYYATN
DNA4(370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKFAKTTWLQAASLLFVDNPVGT
P_AAB.00341	61	SCHNESELPLVMWLQGGEGGSSTGEGNEELGPLDSDLKERETTWLQAASLLEVDNPVGT
DNA40370	101	GFSYVDGSGAYAKDLAMVASDMMVLLKTFFSCHKEFOTVFFYIFSESYGGKMAAGIGLEL
P_AAB.30341	1::1	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFØTVPFYIFSESYGGKMAAGIGLEL
ENA40370		YFAIQEGTIKCHFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
P_AAB.:0341	181	YKAIQEGTIKCHFAGVALGDSWISEVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGU: FEATELWGYAEMIIEONTDGVNFYNILTKSTFTSTMESSLEFTQSHLVCLCQRH
P_AAB.00341	241	VNKGLYEEATELWGKAEMIIEONTDGVNFYNILTKSTPTSTMESSLEFTOSHLVCLCQRH
DNA40370	301	VFHLQEDALSQLMNGPIEKKLKIIFEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
P_AAB.00341	301	VERLOEDALSOLMNOPIEKKLKIIPEDQSWGGQATEVFVNMEEDFMEPVISIVDELLEAG
ENA40370		INVIVENGQLOLIVUINGQEAWVRKLEWPELPKFSQLEWEALYSDPESLETSAFVKSYKN
P_AAB20341	36.1	INVTVINGQLDEIVITMGGEAWVRELEWPELPEFSQLEWEALYSDPESLETSAFVKSYKN
DNA:10370	.;. 1	LAFYW.IKAGHMVP3DQGUMALKHMRIVTQQE
P_AAB.19341	.; 1	LAFYW LKAGHUVPSDQGDMALKUMFLVTQQE
>3 P_AAY=83/3 sequence - Ho	PFO mo s 2 ≀9	LAFYWILKAGHMVPSDQGDMALKMMRIVTQQE 30:, v tellogenic carboxypeptidase honologue amino acid apiens. (45: aa) [1 seg] 22 bit 1. Expect = (.0
>3 P_AAY=83/3 sequence - Ho	∈ PEO mo s 2 +9 = 412	LAFYWILKAGHMVPSDQGDMALKMMRIWTQQE 30:, v tellogenic carboxypertidase honologue amino acid aprens. (45: aa) [1 seg] 22 bit [, Expect = (.0 //452 (10 %), at 1,1-452,452
>3 P_AAY*(3/3 sequence - Ho Score : 238 Identities =	PEO mo s 2 (9 4)2	LAFYWILKAGHMVPSDQGDMALKHMELWTQQE 30:, v tellogenic carboxypertidase homologue amino acid apiens. (45: aa) [1 seg] 22 bit 1, Expect = (.0 /411 (.(0)), Positives = 452/452 (10 ***, at 1,1-452,452 **) MELAL ESPVPRULLIPLIAGENAGENIOWPTEEGEFTWDYVTVRKDAYMFWWLYYATN
>3 P_AAV*83/3 sequence - Ho Score = 238 Identities =	PFO me s 2 (9) 4 2 1	LAFYWILKAGHMVPSDQGDMALKMMRIVTQQE 30:, v tellogenic carboxypeptidase honologue amino acid apiens. (45: aa) [1 seg] 22 bit], Expect = (.0 74:1 (.(0)), Positives = 45:/452 (10 %), at 1,1-452,452 MELAL ESPVPRVILLIPLICALMAGA/TOWPTEEGEF**********************************
>3 P_AAY*(3/3 sequence - Ho Score : 238 Identities =	2PFO mo s 2 (9 4)2 1	LAFYWILKAGHMVPSDQGDMALKMMELVTQQE 30:, v tellogenic carboxypertidase honologue amino acid aprens. (45: aa) [1 seg] 22 bit 1, Espect = (.0 /402 (10 %), at 1,1-452,452 MELAL ESPVPRULLIBELLERIAGATIOWPTEEGEFTUDEVTVREDAYMFWWLYYATN MELAL-ESFVPRWLLLIPELLSLIAGATIOWPTEEGEFTUDEVTVREDAYMFWWLYYATN SCENF EELPLYMWLQGJPGGSSTGFGNFEELGPLDSDLEPRETTWLQAASLLEVDHPVGT
>3 P_AAY*(3/3 sequence - Ho Score : 238 Identities = PAAY*-378	PFO mo s 2 +9 2 1 1 1 + 1 + 1	LAFYWILKAGHMYPSDQGDMALKHMELVTQQE 30:, v tellogenic carboxypeptidase honologue amino acid aprens. (45: aa) [1 seg] 22 bit [, Espect = (.0 //412 (.00), Positives = 452/452 (10 %), at 1,1-452,452 MELAL ESPYPRYLLLIPLLIGHAGA//IDWPTEEGEF-WDYYTVREDAYMFWWLYYATN MELAL-ESPYPRYLLLIPLLIGHAGA//IDWPTEEGEF-WDYYTVREDAYMFWWLYYATN SCHNF ELPLYMWLQGGPGGSSTGFGNFEELGPLDSDLKPRHTTWLQAASLLFVDNPVGT SCHNF ELPLYMWLQGGPGGSSTGFGNFEELGPLDSDLKPRHTTWLQAASLLFVDNPVGT
>3 P_AAY*8373 sequence - Ho Score : 238 Identities = FNA**374 P_AAY*+378 FNA**379	PFO mo s 2 +9 2 1 1 1 +1 1 1 1	LAFYWILKAGHMYPSDQGDMALKHMELWTQQE 30:, v tellogenic carboxypeptidase honologue amino acid aprens. (45: aa) [1 seg] 22 bit [, Expect = (.0 //412 (.00), Positives = 452 (452 (10 %), at 1,1-452,452 //412 (.00)), Positives = 452 (452 (10 %), at 1,1-452,452 //412 (.00)), Positives = 452 (452 (10 %), at 1,4-452 (.00)), Positives = 452 (452 (10 %), at 1,4-452 (.00)),
>3 P_AAY*8378 sequence - Ho Score : 236 Identities = DNA**(37) P_AAY*+378 DNA**(37) P_LAY**378	PFO mo s 2 +9 2 1 1 1 +1 1 1 1	LAFYWILKAGHMYPSDQGDMALKHMELWTQQE 301, v tellogenic carboxypeptidase honologue amino acid aprens. (45: aa) [1 seg] 22 bit [, Espect = (.0 //412 (.00), Positives = 452/452 (10 %), at 1,1-452,452 MELAL ESPYPRYLLLEPLLERLAGY/TOWPTEEGEF/WDYYTYREDAYMFWWLYYATN MELAL-ESPYPRYLLLEPLLE SLUAGY/TOWPTEEGEE/WDYYTYREDAYMFWWLYYATN SCENF SELPL/MWLQGSPGGSSTGFGNFEEISPLDSDLEPRETTWLQAASLLFYDNPYGT SCENF SELPL/MWLQGSPGGSSTGFGNFEEISPLDSDLEPRETTWLQAASLLFYDNPYGT SCENF SELPL/MWLQGSPGGSSTGFGNFEEISPLDSDLEPRETTWLQAASLLFYDNPYGT SCENF SELPL/MWLQGSPGGSSTGFGNFEEISPLDSDLEPRETTWLQAASLLFYDNPYGT
>3 P_AAYF(3/3 sequence - Ho Score = 238 Identities = DNAT(37) P_AAYF(378 DNAT(37) P_LAYF(378 DNAT(37)	PFO me s 2 +9 4 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LAFYW'LKAGHMVPSDQGDMALKMMRLVTQQE 30:, v tellogenic carboxypeptidase honologue amino acid apiens. (45: aa) [1 seg] 22 bit [, Espect = (.0 / /4:: (.0), Positives = 452/452 (10 %), at 1,1-452,452 MELAL ESPVPRWILLIPLINGLIAGA/FIDWPTEEGEFTWDYVTVREDAYMFWWLYYATN MELAL-ESPVPRWILLIPLINGLIAGA/FIDWPTEEGEETWDYVTVREDAYMFWWLYYATN SCENF ELPLYMWLQG JPGGSTTGFGNFEEIGPLDSDLKPRKTTWLQAASLLEVDNPVGT BCKNF ELPLYMWLQG JPGGSTTGFGNFEEIGPLDSDLKPRKTTWLQAASLLEVDNPVGT CSSYLTGLOGAYARBIAMVACDMMYLLETFFSCHKEFOTVEFYIFSESYGGKMAAGIGLEL GESYLTGGGGAYAKDLAMVACDMMYLLETFFSCHKEFOTVEFYIFSESYGGKMAAGIGLEL TWAIDPGTIKCNFAGVALGDSWISPVDSVLSWGFYLYCMSLLEDEGLAEVSKVAEQVLNA
>3 P_AAY*(3/3 sequence - Ho Score : 238 Identities = DNA1*(37) P_AAY*+378 DNA4*(37) P_LAY*A378 DNA4*(37) P_LAY*A378 DNA4*(37) P_LAY*A378	PFO mo s 2 +9 4 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LAFYWILKAGHMVPSDQGDMALKMMELVTQQE 307, v tellogenic carboxypeptidase honologue amino acid apiens. (45: aa) [1 seg] 22 bit [, Expect = (.0 //452 closs), at 1,1-452,452 MELAL ESPVPRULLIPLICALMAGAZIOMPTEEGEFUNDYVTVREDAYMFWWLYYATN MELAL-ESPVPRULLIPLIL BLUAGAZIOMPTEEGEFUNDYVTVREDAYMFWWLYYATN SCKNF EELPLZMWUQG JPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLQAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLGAASLLEVDUPVGT GCKNF EELPLZMWUQGJPGGSSTGFGNFEELSPLDSDLEPRETTWLGAASLLEVGKVAEQVLNA GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
>3 P_AAY+8378 sequence = Ho Score = 238 Identities = FNA+378 P_AAY+378 P_AAY+378 P_LAY**378 DNA+379 P_AAY38378 DNA+379 P_AAY38378 DNA+0370 F_AAY38378	PRO mo s 2 (9 4 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LAFYW'LKAGHMYPSDQGDMALKUMELYTQQE 30F, v tellogenic carboxypeptidase homologue amino acid apiens. (45: aa) [1 seg] 22 bit [, Espect = (.0 /411 (.00), Positives = 450/452 (10 %), at 1,1-458,452 MELAL ESPYPRULLEPLEGEDAGA/YLOWPTEEGEFYEDFYTYREDAYMFWWLTYATN MELAL-ESPYPRULLEPLEGEDAGA/YLOWPTEEGEFYEDFYTYREDAYMFWWLTYATN SCKNF EELPLYMWLQG SPGGSSTGFGNFEELGPLDSDLKPRKTTWLQAASLLEVDHPVGT BCKNF EELPLYMWLQGGPGGSSTGFGNFEELGPLDSDLKPRKTTWLQAASLLEVDHPVGT BCKNF EELPLYMWLQGGPGGSSTGFGNFEELGPLDSDLKPRKTTWLQAASLLEVDNPVGT BSYLTGLYAAABSLAMVAGDDMYGLETFFSCHKEFGTYFFYLFGEGYGGKHAAGIGLEL TMALQSGTIKCNFAGVALGCSWISPVDSVLSWGFYLYEMSLEEDEGLAEVSKVAEQVLNA YUAIGSSTEECHEVGVALGCSWISPVDSVLSWGFYLYEMSLEEDEGLAEVSKVAEQVLNA TUAIGSSTEECHEVGVALGCSWISPVDSVLSWGFYLYEMSLEEDEGLAEVSKVAEQVLNA TUAIGSSTEECHEVGVALGCSWISPVDSVLSWGFYLYEMSLEEDEGLAEVSKVAEQVLNA TUAIGSSTEECHEVGVALGCSWISPVDSVLSWGFYLYEMSLEEDEGLAEVSKVAEQVLNA
>3 P_AAY*(3/3 sequence - Ho Score : 238 Identities = DNA**(37) P_AAY*+378	PFO mmo s 2 (9 4 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LAFYW'LKAGHMYPSDQGDMALKHMELYTQQE 301, v tellogenic carboxypeptidase honologue amino acid apiens. (45: aa) [1 seg] 22 bit 1, Espect = (.0 7412 (.00)), Positives = 452/452 (10 %*, at 1,1-452,452 MELAL ESPYPRULLIPHILAGHAGAYIDWPTEEGEF TOTYTVREDAYMFWWLYYATN MELAL-ESPYPRULLIPHILAGHAGAYIDWPTEEGEF TOTYTVREDAYMFWWLYYATN SCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLEVDHPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLEVDHPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLEVDHPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLEVDNPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRTTWLQAASLLEVDNPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRTTWLQAASLLEVDNPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLDSDLKPRTTWLQAASLLEVDNPVGT GCKNF ELPLYMWLQG SPGGSSTGFGNFEEIGPLAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA

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301 VRHLQFUALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
   P AAY88378
                       361 INVTVYNGQLOLIVETMGQEAWVEKLEWPELPKFSQLKWKALYSEPKSLETSAFVKSYKU
      DNA40370
                               361 INVTVYNGQLDLIVDTMOÇEAWVEKLEWPELPEFSQLKWEALYSDPESLETSAFVKSYKI
   P AAY8837E
                       401 LAFYWIIKAĞHMVPƏDQGEMALKMMRIVTQQE
      DNA40370
                                411 LAFYWILKAGHMVFSDQGDMALKMMRLVTQQE
   P AA788378
>4 P AAY13387 protein PF0302 - Homo sapiers. (452 aa) [1 seg]
 Score = 2382 (922 bate), Expect = 0.0
 Identities = 452/452 (100%), Positives = 451/452 (100%), at 1,1-452,452
                           1 MELALFESPVPFWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
      DNA40370
                               1 MELALFESPVFFWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFKDAYMFWWLYYATN
   P AAY13387
                         61 SCKNESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPEKTTWLQAASLLEVDNPVGT
      DNA40370
                         -61 SCHIFSELPLVNWLQGGPGGSSTGFGHFEELGPLDSDLKPRKTIWLQAASLLFVDNPVGT
   P AAY13387
                        121 GESYVNGSGAYAKOLAMVASDMNULLETFESCHKEFQTVPFYTFSLEYGGKMAAGIGLEL
      ENA40370
                        1111 GESTYNGSGAYAKDLAMVASDMMYLLETFFSCHKEFÇTVPFYIFSESYGGKMAAGIGLEE
   P AAY13387
                        181 TEATOFGTIECMEAGVALGUSWIGPVISVLUWGPYLYSMCLLEDKGLAEVSKVAEQVLNA
      DNA40370
                        181 YEALOFGTIKONFAGVALODSWLSPVESVLSWGPYLYSMSLLEDEGLAEVSKVAEQVLNA
   P AAY13387
                       241 VNEGLYREATELWGFARMLIEONTDGVNFYNLLTESTPTSTMESSLEFTQSHLVCLCQEH
      DNA40370
                                241 AMEGUYREATEI WGKAEMI IEQNTDGUNFYNI DTEST PTSTMESS LEFTQSHLVCLCQEH
   P AAY1338V
                        301 YEHLOFDALSOINMEPEREKLETTPEHOŞWGGQATNUPVNMEEDFHEFVISIVDELLEAG
      DHA40570
                                301 VEHEQEDALSQEMNGPIERKLKIIPEFQSWGGQATNVFVMMEEDFMEFVISIVDELLEAG
   P AA713387
                        351 INTEVENGOLDI I VETINGGEAWYELLEWPELPEFSOLKWEALYSDERSLETSAFVESYEU
      DNA40370
                        361 INVTVYNGOLDI IVPTMGQEAWVEKLEWPELPKFSQI KWEALYSDEKSLETSAFVKSYKU
   P AAY13387
                       41.1 DARYWINKACHOMELO, GIMALRIMBRINIS, QE
      FNA408710
   POWARY NAMED AND ARREST SAME TO BE A PROMISED AND A
>5 P AAY057e8 Human Phosle (vitellogeni: carloxypeptidase homologue) - Homo (452
aa) [1 sed]
                 23-2 (MIN bita), Expect
 Score =
                                                                       - 451745 : (1031), at 1,1-452,452
 Identities 45%/35 http://destrices
                           I MECASER, COLE WOLD DE COLOCIDA COLOMPTER E EUROPYTUELO AMERICAMONATO
      111.4(15)
                          F. Aren Divers
      INAAN KA COO MINEMERE INAMI, KARKONI ARABEERIN MEKERMITWE, AACINEMERSET
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61 SCKNESELPLVMWLOGGPGGSSTGEGNFEEIGPLDSDLKPRKTTWLOAASLLFVDNPVGT
 P AAY05768
              1::1 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
    DNA40370
              1:1 GFSYVNISGAYAFDLAMVASDMMVLLKTFFSCHKEFQTVPFY1FSESYGGFMAAGIGLEL
 P AAY05765
              181 YKATQPOTIKONFAGVALGDSWISFVDSVLSWGFYLYSMSLLEDKGLAEVSKVAEQVLNA
   DNA40370
              181 YEATOF GTIKCNFAGVALGDSWISEVDSVLSWGFYLYSMSLLEDKGLAEVSKVAEQVLNA
 P AAY05768
              241 VNKGLYREATELWGEAEMIJEONTOGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
    DNA40570
              241 VNKGLYFEATELWGFÆEMIJEONTDGVNFYNILTKSTPTSTMESSLEFTOSHLVCLCQEH
  P AAY05766
              301 VEHLQEDALSOLMNOPIRKELEITELOSWGGOATNVEVNMEEDEMKEVISIVDELLEAG
   DNA40370
              301 MEHLQEDALSQLMNGPIRKKLKIIFEDOSWGGOATNVFVNMEEDFMKFVISIVDELLEAG
 P AAYOUTGE
              361 INVTVYNGQLDLIVDTMCQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKU
    DNA 10370
                   **************
              361 INVTVYNGQLOLIVDTMGQEAWVEKLKWPELPRESQLKWKALYSDPESLETSAFVKSYKN
 P AAYOST 64
              4.21 LAFYWILKAGHMVESDQGJMAJHMMRIJUTQQE
   DHA40371
              431 LAFYWILKAGHMVPCDQGDMALKMMELVTQQE
  P AAY 05 For
>6 AAG16692.1 serine darboxypeptidase 1 predursor protein - Homo samiens (45)
aa) [1 seq]
Score = 2382 (923 bits), Expect = 0.0
 Identities = 452/452 (100 ), Positives = 450.452 (100), at 1,1-452,452
                1 MELAGESPYPRWIEDEPGIEGENAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWEYYATN
    DNA40370
               1 MELALRESEVERWILLSELLGGDAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
 AAC16692.1
               61 JCENESELPL/MWLQGGPGGSSTGFGHFEEIGPLDSDLKPRETTWLQAAGLLFVONPVGT
   DNA40370
               51 GCENESELEL/MWLÓG-BEGGSUTGEGEFEÉTGÉLDSDLKPRETTWLQAAGLLEVONPVUT
 AAC16592.1
              121 GET YVNGSGAYAEDLAMVASDMMVLLETFFSCHEEFQTVPFVIFSESYGGKMAAGIGLEL
   EINA40370
              131 GF. YVNGGGAYAKDLAM ASDMMULLKTFFSCHKEFOTVPFYIFSESYGGKMAAGIGLEL
 AAG16692.1
              IVI HVIIÇE TELK MEW TVALGOSWI SEVORVILIWIEFILYSMŠDIEDKGLAEVOKVAEQVINA
   TNA4: 370
              TWY FRATOR TERMINED TTAINGDSWIDEN DUTTERS TO THE BEST LED KOLARVICK VAROND TA
 AACH 6092.1
              241 MEGLYBEATFLWCKAEMELEONTDCCFFFNILTKSTPTSTMESGLEFTOSHLVCLCQEH
   DNA40370
              1341 THROLYPEATELWORAFMITEONTDG/NEYDLLTKSTPYSIMEGGLEFT/GGHLVCLCORH
  AAG16692.1

    1 TREE, FORD SIME SIME SIME SERVING SPATING MEMBERSHES TO INDENDEAG

   INDATE:
              \sigma . Then, is the common the retired that can be a movembre defended to a positive and
  AATHIFFOLL
             or politication, in ilitoo ital, handertarne eleketa, i enkaledita eli elimakukatek
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AAG16692.1 361 INVTVYNGQLDLIVDTMGQEAWVEKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
            421 LAFYWILKAGHMVESDQGDMALKMMPLVTQQE
   DNA40270
                ***********
 AAG16697.1
            4:1 LAFYWILKAGRMVESDOGDMALKMMELVTOOE
>7 NF 067639.1 serine carboxypeptidase 1 poecursor protein - Homo sapiens (452
aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452
              1 MELALERSPVPRWLLLLPELLGENAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
   DNA40370
              1 MELALERSPYPRWLLLLPDDLGDNAGAVIDWPTEEGKEVWDYVTVEKDAYMFWWLYYATN
NP 067639.1
             G1 SCKNESELPLVMWLOGGPGGSSTGFGNFEELGPLDSDLKPEKTTWLQAASLLEVDNPVGT
   DNA40370
                **********
             61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPEKTTWLQAAGLLFVDNPVGT
NP 067639.1
            101 GESYVNGSGAYAKDLAMVASDMMVLLKTFESCHKEFOTVPFYLFSESYGGKMAAGIGLEL
   DNA40370
                ************
            1. 1 GESYVDOSGAYAKDLAMVAEDMMVLLKTFFSCHKEFÇTVPFY1FSESYGGKMAAGIGLEL
NP 067639.1
            1%1 YEATQEGTIKCHFAGVALGOSWIOPVDGVLUWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
   DHA40370
            1:1 YKATOLGTIKCHPAGVALCDSWISPVDGVLJWGPYLYSMSLLEDKGLAETSKVAEQVLMA
NP 067639.1
            241 WERGLYFEATELWGRAEMHIEQNTDGVNFYHILTESTPTSTHESSLEFTQSHLVCLCQRH
   ENA40270
                *************************
            241 VNKGEMERATELUGKARMITEQNTDGVHFYNTLTKSTPTSTMESSLEFTQSHLVCLCQKH
MP 067639.1
            301 VEHLQEDALSQLMNGFIEFELKITFEDDSWGGQATNVFVNMEEDEMKEVISIVDELLEAG
   ENA40 - 70
                *****************
           NOT VEHLQEDALSQLENGETREKLKI FELIQSWGGQATMVEVNMEEDEMEEVISIVDELLEAG
MP 06765+.1
            1001 INTTYYNGOLDLE VOTINGGEAWVEELKWPEEPKFSOI KWKALYSDPESLETSAFVESYKU
   ENA40:/70
            331 INVTVYNGOLDLIVDTMGCEAWVEKLKWPELPKFSOLKWEALYSDPESLETSAFVKSYKU
NP 06763 1.1
            401 LAFYWILKAGHMYPSDQGUMALKHMELYTQQE
   DHA40370
                4:1 LAFYWILKAGHNYPSDQG, MALKUMELNTQQE
NP 06753 +. 1
>8 P AAB4 675 Human OPFK ORF14 of polypeptide requence SEQ ID No. 873 - Homo .451
aa) [1 sec]
       -2506 - 892 \text{ blts}), Expect = 1.0
Score =
Identities = 439/452 (97), Positives = 444/452 (98%), Gapo = 1/452 (0), at
1, 1-452, 4 + 1
              1 MELALBRUEYPENDLELET LEGENACATIONPTEEGFEVWDYVTUF KOAYMEWWLYYATN
   DNA40370
              1 MELALERSEYPPULLELELGEMAGAZIDMETREGKEVWIYYZTURKI AYMEWWLYYATT
 P AAP41-75
             61 . KIPPELPLIKAN, GOP WEDTGFOMFERIGPED DIKPRETTEL, AASLEPVDHPVGT
   DNA40 ITE
             81 PART-DEDUCEMEN, GOI O EOGGEGNEER GREDSCHKERKTTVL, AARLIEVDHRVGT
 P AAE-116 Fe
```

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121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
      EnA40370
                              ************
                       120 GFSYVNGSGAYAKULAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
   P AAB41675
                      181 YMATQPGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
      ENA40370
                       130 YFWIQFGTIECNFAGVALGDSWISFVDSVLGWGPYLTSMCLLEDEGLAEVSEVAEQVLNA
   P AAE41675
                       241 VNKGLYFEATELWGKAEMITEQNTDGVNFYNTLTKSTPTSTMESSLEFTQSHLVCLCQRH
      ENA40370
                       240 VNKGLTE EATELWGKAEMI I EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
   P AAB41675
                       301 VEHLQEDALSQLMNGPIRKKLKTIFEDQSWGGQATNVFVHMEEDFMKPVISIVDELLEAG
      DNA40370
                       300 VEHLQEDALSQLMNGPIREELKTIFEDQSWGGQATNVFVDMEEDFMKFVIDIVDTLLEAG
   P AAB41675
                       361 IDVTVYNGQLDLIVDTMGQËAWVEKLKWPELPKESQLKWFALYSDPESLETSAFVKSYRN
      DDA40370
                               360 VNVTVYNGQLDLIVDTIGQEAWVEKLKWPELSEFNQLKWKALYSDPKSLETSAFVKSYKN
   P AAB41675
      EHA40370
                       4. 1 LAFYWIIKAGHMVESDQGIMALKMMRLYTQQE
   P AAB41675 410 LAFYWILKAGEMVPSDQGIMAEKMMRLVTQQE
>9 AAG39285.1 MUTP084 - Homo sapiens 410 aa) [1 seg]
 Score = 2116 (319 bit: , Expedit = 1.0
 Identities = 402/402 (100%), Positives = 402/402 (100%), at 51,1-452,402
                         51 MPWWLTYATNSCKNESEL:LVMWLQGGPGG.STGFGNFEEIGPLDSDLKPEKTTWLQAAS
      DNA40370
                               1 MEWWLYYATNSCHMESELELVMWLQGGPGGUSTGFGMFEEIGPLDSDLKPEHTTWLQAAS
   AAGB9235.1
                       111 LIFYDDPVOTEPSYVNGSGAYAKDLAMYASDMMVLLETFFSCHFEFQTYPFYIFSESYGG
      DNA40370
                               61 LEFTODPVETGETTVYSSTAYARDIAMVALIMMVLJETFFSCHEFFOTYPFYIFTESYGG
   AAGB9215.1
                      1-1 KMAAS: JULIYKAJORGTIECNFAGVALGUUWISPVOSVLGWGPYLYSNSULEDKGLAEV
      DMA 1370
                       1 :1 KMAAGU GLELYKAIQEGTIKONFAGVALGDUWISPVDSVLSWGPYLYSUSLLEDEGLAEV
   AAG39285.1
                       UBI SEVALOVLMAVNEGLYREATELWGFAEMLIEQNTDGYNFYNILTFSTFTSTMESSLEFTQ
      DNA40370
                               181 OKVABOVICEZIMESI YRZATELMGEALHH LEQUTOSI HEYNH LTESTECSTMECCLEFTQ
   AAG GERG. 1
      DNA 1907 - 191 CHU TEO, KE VERE, KEALCOLIMO PERKEUKI 120 QSW 30A1 NYFYIMEED FILEPYI
                                241 SHLVCLCGFFYERLGEDALSGEMMGPIRKFLKIIPEDQSWGGQATNVFYNMEEDFMKPVI
   AAG39285.1
                       351 SIVDELI-EAGINVIVYNGOLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLE
      DNA40370
                               * TO THE ADMINISTRACTION OF THE ADMINISTRACY PROPERTY OF THE ADMINISTRACTION OF THE ADMI
   AAGRWY 45.1
      ONATO - 5 411 COMERCIONED MERCINE PARTECIO DI COLHADE IMPLATO, E
                       i ek jaron da kalangan kangan kanan ka
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